

## SEQUENCE LISTING

<110> Biogen Idec MA Inc.  
Prentice, Holly

<120> HIGH EXPRESSION LOCUS VECTOR BASED ON  
FERRITIN HEAVY CHAIN GENE LOCUS

<130> 2159.058PC01/EKS/LMB

<140> PCT/US2003/033433  
<141> 2003-10-22

<150> US 60/421,252  
<151> 2002-10-24

<160> 41

<170> FastSEQ for Windows Version 4.0

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ccggagcgcg cctgacgcag gatcccgcta taaagtgcgg cccgctgtc cctacgcccag 180  
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gctcgacccc tccgaccccc gtccggccgc tttgagcctg agcccttgc aacttcgtcg 300  
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Met Thr Thr Ala  
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tct ccc tcg caa gtg cgc cag aac tac cac cag gac tcg gag gct gcc 405  
Ser Pro Ser Gln Val Arg Gln Asn Tyr His Gln Asp Ser Glu Ala Ala  
5 10 15 20

atc aac cgc cag atc aac ctg gag ttg tat gcc tcc tac gtc tat ctg 453  
Ile Asn Arg Gln Ile Asn Leu Glu Leu Tyr Ala Ser Tyr Val Tyr Leu  
25 30 35

tcc atg gtgagtgccgg cctggccttt gcggggggccgg aaagagggtg cggcctggcc 509  
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<213> Rattus norvegicus

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 Tyr Val Tyr Leu Ser Met  
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 taggaggcat acaactccag gttgatctgg cgggtatgg cagcctccga gtccctgggtgg 180  
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<220>  
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 Tyr Phe Asp Arg Asp Asp Val Ala Léu Lys Asn Phe Ala Lys Tyr Phe  
 5 10 15

ctc cat caa tct cat gaa gag agg gaa cat gct gag aaa ctg atg aag 152  
 Leu His Gln Ser His Glu Glu Arg Glu His Ala Glu Lys Leu Met Lys  
 20 25 30

ctg cag aac cag cga ggt gga cga atc ttc ctg cag gat atc aag 197  
 Leu Gln Asn Gln Arg Gly Gly Arg Ile Phe Leu Gln Asp Ile Lys  
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<210> 5  
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tgtatggagaa agtatttggc aaagttcttc agggccacat catcccggtc	aaaataacaa	180
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Glu Ser Gly Leu Asn Ala Met Arg Cys Ala Leu His Leu Glu Lys Ser		
10 15 20		

gtg aat cag tca cta ctg gaa ctt cac aaa ctg gct act gac aag aat		150
Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn		
25 30 35		

gat ccc cac gtgagtatca gaaacacggg gtgagtgag atgatttgcc		199
Asp Pro His		
40		

acagggcttg ggagagctga ccagtaaccc tgccttcatgt tctctttcct ag tta tgt		257
	Leu Cys	

gac ttc att gag acg cat tac ctg aat gag cag gtg aaa tcc att aaa		305
Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys Ser Ile Lys		
45 50 55 60		

gaa ctg ggt gac cac gtg acc aac tta cgc aag atg gga gcc cct gaa		353
Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly Ala Pro Glu		
65 70 75		

tct ggc atg gca gaa tat ctc ttt gac aag cac acc ctg gga cac ggt		401
Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly		
80 85 90		

gat gag agc taa gctgacgtcc ccaaggccat gtgactttac tggctcactg	453
Asp Glu Ser *	
95	
aggcagtgc a tgcatgtcag gctgcctt a tctttctat aagttgcacc aaaacatctg	513
cttaaaagt ctttaattt taccatttct tcaaataaaag aattttggta cccagctctt	573
gttgtgattt aggatgagcg caccagctt ccttgcgtcg gctatataac cacactgcaa	633
cgcctgaaag aatattttt aaactcgtag ttggggaaag atagtgaaag acaggtgtgt	693
tcagacagga ctaagcagtc ctggttctga gttacctgcc agactgccat gggAACATAT	753
tcttgagtgt c	764
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Lys Leu Ala Thr Asp Lys Asn Asp Pro His	
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His Gly Asp Glu Ser	
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tctttcaggc gttcagttt gtttatatacg ccgacgcaag ggaagctggc gcgctcatcc	180
tcaatcacaa caagagctgg gtaccaaaat tctttatttgc aagaaatggc acaaattaaa	240
gaactttaa gcagatgtt tggcactatatacg ataaaggccat cctgacatgc	300
atgcactgccc tcagtgcgccc agttaaagtca catggccttgc gggacgtcag cttagctctc	360
atcaccgtgt cccagggtgt gcttgcataa gagatattct gccatgccat attcaggggc	420
tcccatcttgc gtaagggtgg tcacgtggc acccagttct ttaatggatt tcacctgctc	480
attcaggtaa tgcgtctcaa tgaagtcaca taactaggaa agagaacatgc ggacagggtt	540
actggtcagc tctcccaagc cctgtggcaa atcatcttca ctcaccccgat tttctgata	600
ctcacgtggc gatcattttt gtcagtagcc agtttgcataa gttccagtag tgactgattc	660
acactctttt ccaagtgcag tgcacacacccatca attgcattca gcccgccttc ccagtcatca	720
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60 65 70	
agt gtg aat cag tca cta ctg gaa ctt cac aaa ctg gct act gac aag	1610
Ser Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys	
75 80 85	
aat gat ccc cac gtgagtatca gaaacacggg gtgagtgag atgatttgcc	1662
Asn Asp Pro His	
90	
acagggcttg ggagagctga ccagtaaccc tgcgttcatgt tctctttcct ag tta tgt	1720
Leu Cys	
gac ttc att gag acg cat tac ctg aat gag cag gtg aaa tcc att aaa	1768
Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys Ser Ile Lys	
95 100 105 110	
gaa ctg ggt gac cac gtg acc aac tta cgc aag atg gga gcc cct gaa	1816
Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly Ala Pro Glu	
115 120 125	
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Ser Gly Met Ala Glu Tyr Leu Phe Asp Lys His Thr Leu Gly His Gly	
130 135 140	
gat gag agc taagctgacg tccccaaaggc catgtgactt tactggtcac	1913
Asp Glu Ser	
145	
tgaggcagtg catgcgttc aggctgcctt tatctttctt ataagttgca ccaaaacatc	1973
tgcttaaaag ttcttaatt tgtaccattt cttcaaataa agaattttgg tacccagctc	2033
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Met Lys Leu Gln Asn Gln Arg Gly Gly Arg Ile Phe Leu Gln Asp Ile	
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Lys	
<210> 13	
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<400> 13

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							20			25				30	
Lys	Leu	Ala	Thr	Asp	Lys	Asn	Asp	Pro	His						
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<211> 53

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetically generated peptide

<400> 14

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							5			10				15	
Ile	Lys	Glu	Leu	Gly	Asp	His	Val	Thr	Asn	Leu	Arg	Lys	Met	Gly	Ala
							20			25				30	
Pro	Glu	Ser	Gly	Met	Ala	Glu	Tyr	Leu	Phe	Asp	Lys	His	Thr	Leu	Gly
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<212> DNA

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caaccctgca	gttaggtgca	ttttcctgca	ctctcgtccc	ctccggtcac	atggcctgca	360
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gcattgaaac	ttatcgctag	aatctcccc	ttctgtatac	accctgacct	tgccaaggca	600
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<211> 191

<212> DNA

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gcttaaaagt tcttaattt gtaccatttc ttcaaataaa gaatttttgt acccagctct	180
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<212> DNA

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<210> 18

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<213> Artificial Sequence

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 His Gln Asp Ser Glu Ala Ala Ile Asn Arg Gln Ile Asn Leu Glu Leu  
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tat gcc tcc tac gtc tat ctg tcc atg gtgagtgcgg cct  
 Tyr Ala Ser Tyr Val Tyr Leu Ser Met  
 30 35

<210> 20  
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 Tyr Val Tyr Leu Ser Met  
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<211> 59
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<210> 29
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<220>
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<400> 29
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<210> 30
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<210> 41
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<400> 41
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